

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/6/6,009  
Source: 1Fw16  
Date Processed by STIC: 9/2/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/6/6,009

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2        Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3        Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4        Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5        Variable Length     Sequence(s)        contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6        PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7        Skipped Sequences  
    (OLD RULES)     Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence:  
                                   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   (i)       SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   This sequence is intentionally skipped  
  
                                   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8        Skipped Sequences  
    (NEW RULES)     Sequence(s)        missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                                   <210> sequence id number  
                                   <400> sequence id number  
                                   000
  
- 9        Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                                   Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                                   In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10        Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11        Use of <220>     Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses.  
                                   Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12        PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13        Misuse of n/Xaa     "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFW16

## RAW SEQUENCE LISTING

DATE: 09/02/2005

PATENT APPLICATION: US/10/616,009

TIME: 14:08:22

Input Set : D:\ISIS-5138.ST25.txt

Output Set: N:\CRF4\09022005\J616009.raw

3 <110> APPLICANT: Crooke, Stanley T.  
 4 Lima, Walter F.  
 5 Wu, Hongjiang  
 7 <120> TITLE OF INVENTION: HUMAN RNASE H1 AND OLIGONUCLEOTIDE COMPOSITIONS THEREOF  
 9 <130> FILE REFERENCE: ISIS-5138  
 11 <140> CURRENT APPLICATION NUMBER: US 10/616,009  
 12 <141> CURRENT FILING DATE: 2003-07-08  
 14 <150> PRIOR APPLICATION NUMBER: US 09/409,926  
 15 <151> PRIOR FILING DATE: 1999-09-30  
 17 <160> NUMBER OF SEQ ID NOS: 72  
 19 <170> SOFTWARE: PatentIn version 3.3  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 286  
 23 <212> TYPE: PRT  
 24 <213> ORGANISM: Human  
 26 <400> SEQUENCE: 1  
 28 Met Ser Trp Leu Leu Phe Leu Ala His Arg Val Ala Leu Ala Ala Leu  
 29 1 5 10 15  
 32 Pro Cys Arg Arg Gly Ser Arg Gly Phe Gly Met Phe Tyr Ala Val Arg  
 33 20 25 30  
 36 Arg Gly Arg Lys Thr Gly Val Phe Leu Thr Trp Asn Glu Cys Arg Ala  
 37 35 40 45  
 40 Gln Val Asp Arg Phe Pro Ala Ala Arg Phe Lys Lys Phe Ala Thr Glu  
 41 50 55 60  
 44 Asp Glu Ala Trp Ala Phe Val Arg Lys Ser Ala Ser Pro Glu Val Ser  
 45 65 70 75 80  
 48 Glu Gly His Glu Asn Gln His Gly Gln Glu Ser Glu Ala Lys Pro Gly  
 49 85 90 95  
 52 Lys Arg Leu Arg Glu Pro Leu Asp Gly Asp Gly His Glu Ser Ala Gln  
 53 100 105 110  
 56 Pro Tyr Ala Lys His Met Lys Pro Ser Val Glu Pro Ala Pro Pro Val  
 57 115 120 125  
 60 Ser Arg Asp Thr Phe Ser Tyr Met Gly Asp Phe Val Val Val Tyr Thr  
 61 130 135 140  
 64 Asp Gly Cys Cys Ser Ser Asn Gly Arg Arg Lys Pro Arg Ala Gly Ile  
 65 145 150 155 160  
 68 Gly Val Tyr Trp Gly Pro Gly His Pro Leu Asn Val Gly Ile Arg Leu  
 69 165 170 175  
 72 Pro Gly Arg Gln Thr Asn Gln Arg Ala Glu Ile His Ala Ala Cys Lys  
 73 180 185 190  
 76 Ala Ile Glu Gln Ala Lys Thr Gln Asn Ile Asn Lys Leu Val Leu Tyr  
 77 195 200 205  
 80 Thr Asp Ser Met Phe Thr Ile Asn Gly Ile Thr Asn Trp Val Gln Gly

Does Not Comply  
Corrected Diskette Needed

P.5

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Input Set : D:\ISIS-5138.ST25.txt

Output Set: N:\CRF4\09022005\J616009.raw

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81      210      215      220
84 Trp Lys Lys Asn Gly Trp Lys Thr Ser Ala Gly Lys Glu Val Ile Asn
85 225      230      235      240
88 Lys Glu Asp Phe Val Ala Leu Glu Arg Leu Thr Gln Gly Met Asp Ile
89      245      250      255
92 Gln Trp Met His Val Pro Gly His Ser Gly Phe Ile Gly Asn Glu Glu
93      260      265      270
96 Ala Asp Arg Leu Ala Arg Glu Gly Ala Lys Gln Ser Glu Asp
97      275      280      285
100 <210> SEQ ID NO: 2
101 <211> LENGTH: 293
102 <212> TYPE: PRT
103 <213> ORGANISM: Chicken
105 <400> SEQUENCE: 2
107 Met Leu Arg Trp Leu Val Ala Leu Leu Ser His Ser Cys Phe Val Ser
108 1      5      10      15
111 Lys Gly Gly Gly Met Phe Tyr Ala Val Arg Lys Gly Arg Gln Thr Gly
112      20      25      30
115 Val Tyr Arg Thr Trp Ala Glu Cys Gln Gln Gln Val Asn Arg Phe Pro
116      35      40      45
119 Ser Ala Ser Phe Lys Lys Phe Ala Thr Glu Lys Glu Ala Trp Ala Phe
120      50      55      60
123 Val Gly Ala Gly Pro Pro Asp Gly Gln Gln Ser Ala Pro Ala Glu Thr
124 65      70      75      80
127 His Gly Ala Ser Ala Val Ala Gln Glu Asn Ala Ser His Arg Glu Glu
128      85      90      95
131 Pro Glu Thr Asp Val Leu Cys Cys Asn Ala Cys Lys Arg Pro Tyr Glu
132      100      105      110
135 Gln Ser Thr Asn Glu Glu His Thr Val Arg Arg Ala Lys His Asp Glu
136      115      120      125
139 Glu Gln Ser Thr Pro Val Val Ser Glu Ala Lys Phe Ser Tyr Met Gly
140      130      135      140
143 Glu Phe Ala Val Val Tyr Thr Asp Gly Cys Cys Ser Gly Asn Gly Arg
144 145      150      155      160
147 Asn Arg Ala Arg Ala Gly Ile Gly Val Tyr Trp Gly Pro Gly His Pro
148      165      170      175
151 Leu Asn Ile Ser Glu Arg Leu Pro Gly Arg Gln Thr Asn Gln Arg Ala
152      180      185      190
155 Glu Ile His Ala Ala Cys Lys Ala Ile Glu Gln Ala Lys Ser Gln Asn
156      195      200      205
159 Ile Lys Lys Leu Ile Ile Tyr Thr Asp Ser Lys Phe Thr Ile Asn Gly
160      210      215      220
163 Ile Thr Ser Trp Val Glu Asn Trp Lys Thr Asn Gly Trp Arg Thr Ser
164 225      230      235      240
167 Ser Gly Gly Ser Val Ile Asn Lys Glu Asp Phe Gln Lys Leu Asp Ser
168      245      250      255
171 Leu Ser Lys Gly Ile Glu Ile Gln Trp Met His Ile Pro Gly His Ala
172      260      265      270
175 Gly Phe Gln Gly Asn Glu Glu Ala Asp Arg Leu Ala Arg Glu Gly Ala

```

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Input Set : D:\ISIS-5138.ST25.txt

Output Set: N:\CRF4\09022005\J616009.raw

```

176          275          280          285
179 Ser Lys Gln Lys Leu
180      290
183 <210> SEQ ID NO: 3
184 <211> LENGTH: 348
185 <212> TYPE: PRT
186 <213> ORGANISM: Yeast
188 <400> SEQUENCE: 3
190 Met Ala Arg Gln Gly Asn Phe Tyr Ala Val Arg Lys Gly Arg Glu Thr
191 1          5          10          15
194 Gly Ile Tyr Asn Thr Trp Asn Glu Cys Lys Asn Gln Val Asp Gly Tyr
195      20          25          30
198 Gly Gly Ala Ile Tyr Lys Lys Phe Asn Ser Tyr Glu Gln Ala Lys Ser
199      35          40          45
202 Phe Leu Gly Gln Pro Asn Thr Thr Ser Asn Tyr Gly Ser Ser Thr His
203      50          55          60
206 Ala Gly Gly Gln Val Ser Lys Pro His Thr Thr Gln Lys Arg Val His
207 65          70          75          80
210 Arg Arg Asn Arg Pro Leu His Tyr Ser Ser Leu Thr Ser Ser Ser Ala
211      85          90          95
214 Cys Ser Ser Leu Ser Ser Ala Asn Thr Asn Thr Phe Tyr Ser Val Lys
215      100         105         110
218 Ser Asn Val Pro Asn Ile Glu Ser Lys Ile Phe Asn Asn Trp Lys Asp
219      115         120         125
222 Cys Gln Ala Tyr Val Lys His Lys Arg Gly Ile Thr Phe Lys Lys Phe
223      130         135         140
226 Glu Asp Gln Leu Ala Ala Glu Asn Phe Ile Ser Gly Met Ser Ala His
227 145         150         155         160
230 Asp Tyr Lys Leu Met Asn Ile Ser Lys Glu Ser Phe Glu Ser Lys Tyr
231      165         170         175
234 Lys Leu Ser Ser Asn Thr Met Tyr Asn Lys Ser Met Asn Val Tyr Cys
235      180         185         190
238 Asp Gly Ser Ser Phe Gly Asn Gly Thr Ser Ser Ser Arg Ala Gly Tyr
239      195         200         205
242 Gly Ala Tyr Phe Glu Gly Ala Pro Glu Glu Asn Ile Ser Glu Pro Leu
243      210         215         220
246 Leu Ser Gly Ala Gln Thr Asn Asn Arg Ala Glu Ile Glu Ala Val Ser
247 225         230         235         240
250 Glu Ala Leu Lys Lys Ile Trp Glu Lys Leu Thr Asn Glu Lys Glu Lys
251      245         250         255
254 Val Asn Tyr Gln Ile Lys Thr Asp Ser Glu Tyr Val Thr Lys Leu Leu
255      260         265         270
258 Asn Asp Arg Tyr Met Thr Tyr Asp Asn Lys Lys Leu Glu Gly Leu Pro
259      275         280         285
262 Asn Ser Asp Leu Ile Val Pro Leu Val Gln Arg Phe Val Lys Val Lys
263      290         295         300
266 Lys Tyr Tyr Glu Leu Asn Lys Glu Cys Phe Lys Asn Asn Gly Lys Phe
267 305         310         315         320
270 Gln Ile Glu Trp Val Lys Gly His Asp Gly Asp Pro Gly Asn Glu Met

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```

271          325          330          335
274 Ala Asp Phe Leu Ala Lys Lys Gly Ala Ser Arg Arg
275          340          345
278 <210> SEQ ID NO: 4
279 <211> LENGTH: 155
280 <212> TYPE: PRT
281 <213> ORGANISM: E.coli
283 <400> SEQUENCE: 4
285 Met Leu Lys Gln Val Glu Ile Phe Thr Asp Gly Ser Cys Leu Gly Asn
286 1          5          10          15
289 Pro Gly Pro Gly Gly Tyr Gly Ala Ile Leu Arg Tyr Arg Gly Arg Glu
290          20          25          30
293 Lys Thr Phe Ser Ala Gly Tyr Thr Arg Thr Thr Asn Asn Arg Met Glu
294          35          40          45
297 Leu Met Ala Ala Ile Val Ala Leu Glu Ala Leu Lys Glu His Cys Glu
298          50          55          60
301 Val Ile Leu Ser Thr Asp Ser Gln Tyr Val Arg Gln Gly Ile Thr Gln
302 65          70          75          80
305 Trp Ile His Asn Trp Lys Lys Arg Gly Trp Lys Thr Ala Asp Lys Lys
306          85          90          95
309 Pro Val Lys Asn Val Asp Leu Trp Gln Arg Leu Asp Ala Ala Leu Gly
310          100         105         110
313 Gln His Gln Ile Lys Trp Glu Trp Val Lys Gly His Ala Gly His Pro
314          115         120         125
317 Glu Asn Glu Arg Cys Asp Glu Leu Ala Arg Ala Ala Ala Met Asn Pro
318          130         135         140
321 Thr Leu Glu Asp Thr Gly Tyr Gln Val Glu Val
322 145         150         155
325 <210> SEQ ID NO: 5
326 <211> LENGTH: 216
327 <212> TYPE: PRT
328 <213> ORGANISM: Mouse EST
330 <400> SEQUENCE: 5
332 Gly Ile Cys Gly Leu Gly Met Phe Tyr Ala Val Arg Arg Gly Arg Arg
333 1          5          10          15
336 Pro Gly Val Phe Leu Ser Trp Ser Glu Cys Lys Ala Gln Val Asp Arg
337          20          25          30
340 Phe Pro Ala Ala Arg Phe Lys Lys Phe Ala Thr Glu Asp Glu Ala Trp
341          35          40          45
344 Ala Phe Val Arg Ser Ser Ser Ser Pro Asp Gly Ser Lys Gly Gln Glu
345          50          55          60
348 Ser Ala His Glu Gln Lys Ser Gln Ala Lys Thr Ser Lys Arg Pro Arg
349 65          70          75          80
352 Glu Pro Leu Val Val Val Tyr Thr Asp Gly Cys Cys Ser Ser Asn Gly
353          85          90          95
356 Arg Lys Arg Ala Arg Ala Gly Ile Gly Val Tyr Trp Gly Pro Gly His
357          100         105         110
360 Pro Leu Asn Val Arg Ile Arg Leu Pro Gly Arg Gln Thr Asn Gln Arg
361          115         120         125

```

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Input Set : D:\ISIS-5138.ST25.txt

Output Set: N:\CRF4\09022005\J616009.raw

364 Ala Glu Ile His Ala Ala Cys Lys Ala Val Met Gln Ala Lys Ala Gln  
 365 130 135 140  
 368 Asn Ile Ser Lys Leu Val Leu Tyr Thr Asp Ser Met Phe Thr Ile Asn  
 369 145 150 155 160  
 372 Gly Ile Thr Asn Trp Val Gln Gly Trp Lys Lys Asn Gly Trp Arg Thr  
 373 165 170 175  
 376 Ser Thr Gly Lys Asp Val Ile Asn Lys Glu Asp Phe Met Glu Leu Asp  
 377 180 185 190  
 380 Glu Leu Thr Gln Gly Met Asp Ile Gln Trp Met His Ile Pro Gly His  
 381 195 200 205  
 384 Ser Gly Phe Val Gly Asn Glu Glu  
 385 210 215

388 &lt;210&gt; SEQ ID NO: 6

389 &lt;211&gt; LENGTH: 26

390 &lt;212&gt; TYPE: DNA

391 &lt;213&gt; ORGANISM: DNA

393 &lt;400&gt; SEQUENCE: 6

394 acgctggccg ggagtcgaaa tgcttc

26

397 &lt;210&gt; SEQ ID NO: 7

398 &lt;211&gt; LENGTH: 28

399 &lt;212&gt; TYPE: DNA

400 &lt;213&gt; ORGANISM: DNA

402 &lt;400&gt; SEQUENCE: 7

403 ctgttcctgg cccacagagt cgccttgg

28

406 &lt;210&gt; SEQ ID NO: 8

407 &lt;211&gt; LENGTH: 29

408 &lt;212&gt; TYPE: DNA

409 &lt;213&gt; ORGANISM: DNA

411 &lt;400&gt; SEQUENCE: 8

412 ggtctttctg acctggaatg agtgcagag

29

415 &lt;210&gt; SEQ ID NO: 9

416 &lt;211&gt; LENGTH: 29

417 &lt;212&gt; TYPE: DNA

418 &lt;213&gt; ORGANISM: DNA

420 &lt;400&gt; SEQUENCE: 9

421 cttgcctggt ttgcacctcc gattcttgt

29

424 &lt;210&gt; SEQ ID NO: 10

425 &lt;211&gt; LENGTH: 29

426 &lt;212&gt; TYPE: DNA

427 &lt;213&gt; ORGANISM: DNA

429 &lt;400&gt; SEQUENCE: 10

430 ttgattttca tgcccttctg aaacttccg

29

433 &lt;210&gt; SEQ ID NO: 11

434 &lt;211&gt; LENGTH: 34

435 &lt;212&gt; TYPE: DNA

436 &lt;213&gt; ORGANISM: DNA

438 &lt;400&gt; SEQUENCE: 11

439 cctcatctc tatggcaaac ttcttaaadc tggc

34

442 &lt;210&gt; SEQ ID NO: 12

*invalid response - see item 10 on Error Summary Sheet*

*same error*

*Please correct this error in subsequent sequences*

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/616,009

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TIME: 14:08:23

Input Set : D:\ISIS-5138.ST25.txt

Output Set: N:\CRF4\09022005\J616009.raw